

TITLE

PLANT AMINOACYL-tRNA SYNTHETASE

ABSTRACT OF THE DISCLOSURE

This invention relates to an isolated nucleic acid fragment encoding an  
5 aminoacyl-tRNA synthetase. The invention also relates to the construction of a chimeric  
gene encoding all or a portion of the aminoacyl-tRNA synthetase, in sense or antisense  
orientation, wherein expression of the chimeric gene results in production of altered levels of  
the aminoacyl-tRNA synthetase in a transformed host cell.

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35

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WRM/bjm

UNITED STATES PATENT AND TRADEMARK OFFICE  
DOCUMENT CLASSIFICATION BARCODE SHEET



# Sequence Listing

9

A large, stylized number '9' is centered on the page, composed of a dense pattern of small dots.

Level - 2  
Version 1.1

SEQUENCE LISTING

<110> Falco, S. Carl  
Famodu, Layo O.  
Orozco, Buddy  
Schwaber, James S.

<120> Plant Aminoacyl-tRNA Synthetase

<130> BB-1193

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<150> 60/093,530  
<151> July 21, 1998

<160> 37

<170> Microsoft Office 97

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35 40 45

His Ala Leu Asn Thr Leu Phe Glu Val Leu Phe Thr Leu Cys Arg Gly  
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His Phe Leu Pro Phe Pro Asp Val Arg Glu Glu Leu Phe Asp Glu Glu  
100 105 110

Val Glu Arg Arg Val Gly Arg Met Gln Arg Val Ile Glu Leu Ala Arg  
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Asp Asn Leu Thr Asn Ile Tyr Val Arg Phe Asn Arg Lys Arg Leu Lys  
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Gly Arg Ser Gly Glu Glu Asp Cys Arg Ile Ala Leu Ser Thr Leu Tyr  
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35 40 45

Val Asp Asp Asp Gly His Phe Ile Glu Lys Ile Ser Gln Phe Lys Gly  
50 55 60

Arg His Val Lys Glu Ala Asp Lys Asp Ile Ile Asn Ala Val Lys Asp  
65 70 75 80

Lys Gly Arg Leu Val Ser Lys Gly Ser Ile Glu His Ser Tyr Pro Tyr  
85 90 95

Cys Trp Arg Ser Gly Thr Pro Leu Ile Tyr Arg Ala Val Pro Ser Trp  
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Phe Ile Lys Val Glu Lys Ile Arg Asp Gln Leu Leu Glu Cys Asn Lys  
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Glu Thr Tyr Trp Val Pro Asp Tyr Val Lys Glu Lys Arg Phe His Asn  
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Arg Leu Lys Glu Glu Lys Lys Asn Lys Ala Ala Ala Ser Gly			
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Lys Pro Gln Lys Ala Ser Ala Ala Asp Asp Asp Asp Met Asp Pro Thr			
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Gln Tyr Tyr Glu Asn Arg Leu Lys Ala Leu Asp Ser Leu Lys Ala Thr			
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Glu Tyr Ile Glu Lys Tyr Arg Thr Leu Ser Glu Gly Glu Lys Leu Thr			
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 Gly Ile Asp Leu Thr His Asn Pro Glu Phe Thr Thr Cys Glu Phe Tyr  
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 His Ala Asn Gly Val Thr Asn Pro Pro Ile Glu Ile Asp Phe Thr Pro  
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Gly Gly Leu Asp Arg Val Tyr Glu Ile Gly Lys Gln Phe Arg Asn Glu  
 50 55 60

Gly Ile Asp Leu Thr His Asn Pro Glu Phe Thr Thr Cys Glu Phe Tyr  
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Met Ala Tyr Ala Asp Tyr Asn Asp Leu Ile Glu Leu Thr Glu Thr Met  
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Leu Lys Tyr Leu Ala Val Gln Lys Ala Glu Gly Asn Asn Pro Tyr Pro  
85 90 95

His Lys Phe Phe Val Thr Met Ser Leu Asp Gln Tyr Ile Lys Glu Tyr  
100 105 110

Gly Gly Leu Ser Asn Gly Gln His Leu Glu Asp Val Ser Val Ser Met  
115 120 125

Ala Gly Arg Ile Met His Lys Arg Thr Ser Gly Ser Lys Leu Val Phe  
130 135 140

Tyr Asp Leu His Ser Gly Gly Phe Lys Val Gln Val Met Ala Asp Ala  
145 150 155 160

Ser Lys Ser Asp Leu Asp Glu Ala Glu Phe Ser Lys Phe His Ser Asn  
165 170 175

Val Lys Arg Gly Asp Ile Val Gly Ile Thr Gly Phe Pro Gly Lys Ser  
180 185 190

Lys Lys Gly Glu Leu Ser Ile Phe Pro Lys Thr Phe Val Leu Leu Ser  
 195 200 205  
 His Cys Leu His Met Met Pro Arg Gln Lys Ser Ala Ala Ala Ala Asp  
 210 215 220  
 Asn Ala Asn Leu Lys Lys Asn Pro Trp Val Pro Gly Ser Thr Arg Asn  
 225 230 235 240  
 Pro Glu Thr Tyr Ile Leu Lys Asp Gln Glu Thr Arg Tyr Arg Arg His  
 245 250 255  
 Leu Asp Leu Met Leu Asn Pro Glu Val Arg Glu Ile Phe Lys Thr Arg  
 260 265 270  
 Ser Lys Ile Ile Cys Tyr Ile Arg Arg Phe Leu Asp Asp Leu Asp Phe  
 275 280 285  
 Leu Glu Val Glu Thr Pro Met Met Asn Met Ile Ala Gly Gly Ala Ala  
 290 295 300  
 Ala Arg Pro Phe Val Thr His His Asn Asp Leu Asn Met Arg Leu Phe  
 305 310 315 320  
 Met Arg Ile Ala Pro Glu Leu Tyr Leu Lys Glu Leu Val Val Gly Gly  
 325 330 335  
 Leu Asp Arg Val Tyr Glu Ile Gly Lys Gln Phe Arg Asn Glu Gly Ile  
 340 345 350  
 Asp Leu Thr His Asn Pro Glu Phe Thr Thr Cys Glu Phe Tyr Met Ala  
 355 360 365  
 Tyr Lys Asp Tyr Asn Asp Leu Met Asp Ile Thr Glu Gln Met Leu Ser  
 370 375 380  
 Gly Met Val Lys Glu Leu Thr Xaa Xaa Xaa Tyr Lys Ile Lys Tyr His  
 385 390 395 400  
 Ala Asp Gly Ile Asp Lys Glu Pro Ile Glu Ile Asp Phe Thr Pro Pro  
 405 410 415  
 Phe Arg Arg Ile Asp Met Ile Asp Glu Leu Glu Lys Val Ala Gly Leu  
 420 425 430  
 Ser Ile Pro Lys Asp Leu Ser Ser Glu Glu Ala Asn Gln Tyr Leu Lys  
 435 440 445  
 Asp Thr Cys Leu Lys Tyr Glu Ile Lys Cys Pro Pro Pro Glu Thr Thr  
 450 455 460  
 Ala Arg Leu Leu Asp Lys Leu Val Gly His Phe Leu Glu Glu Thr Cys  
 465 470 475 480  
 Val Asn Pro Thr Phe Ile Ile Asn His Pro Glu Ile Met Ser Pro Leu  
 485 490 495  
 Ala Lys Trp His Arg Ser Lys Arg Gly Leu Thr Glu Arg Phe Glu Leu  
 500 505 510

Phe Val Asn Lys His Glu Leu Cys Asn Ala Tyr Thr Glu Leu Asn Asp  
515 520 525

Pro Val Val Gln Arg Gln Arg Phe Ala Glu Gln Leu Lys Asp Arg Gln  
530 535 540

Ser Gly Asp Asp Glu Ala Met Ala Phe Asp Glu Thr Phe Cys Thr Ala  
545 550 555 560

Leu Glu Tyr Gly Leu Pro Pro Thr Gly Gly Trp Gly Leu Gly Ile Asp  
565 570 575

Arg Leu Thr Met Leu Leu Thr Asp Ser Gln Asn Ile Lys Glu Val Leu  
580 585 590

Leu Phe Pro Ala Met Lys Pro  
595

<210> 15

<211> 702

<212> DNA

<213> Triticum aestivum

<400> 15

gcacgaggct tgacaagcta gtggccatt tcttggagga aacatgtgtg aacccaacat 60  
ttatttatcaa ccacccagag ataatgagtc cattggcaaa gtggcatagg tcccgacactg 120  
ggttgacaga aagggttgag ctctttgtta acaaacacga ggtgtgcaat gcctacactg 180  
agttaacga tcctgttgtg caaaggcaac gggttgagga acaaactaaag gatcgtcaat 240  
ctgggtatga tgaagctatg gctttggacg aaacattctg cactgccctc gagtatggc 300  
tgccctccgac aggtgggtgg gggttgggaa ttgatcgct tacaatgatg ctgacagatt 360  
cccagaacat caaggaagtt ctcttggtcc cggccatgaa gccccaagag tagctgtttg 420  
caagcccatc aacagagtaa ttttgggttg ctgcgcgtgag gtggaggat tatgacatgt 480  
gacaatacaa cgagtttaa ctgtgccgga caaaaacatgt gttagcagcac tggaggtaca 540  
agctacttt gcgttggaaagg gttgttggaaa atttgaactc cggttaggag gaagagttag 600  
gcatatgaag caagaatcag aaggagacag tgtgctacat gtttgcgttgt tttcttttg 660  
gaagatcaaa atttagtgct tggattgtt atacactttt tt 702

<210> 16

<211> 136

<212> PRT

<213> Triticum aestivum

<400> 16

Thr Arg Leu Asp Lys Leu Val Gly His Phe Leu Glu Glu Thr Cys Val  
1 5 10 15

Asn Pro Thr Phe Ile Ile Asn His Pro Glu Ile Met Ser Pro Leu Ala  
20 25 30

Lys Trp His Arg Ser Arg Pro Gly Leu Thr Glu Arg Phe Glu Leu Phe  
35 40 45

Val Asn Lys His Glu Val Cys Asn Ala Tyr Thr Glu Leu Asn Asp Pro  
50 55 60

Val Val Gln Arg Gln Arg Phe Glu Glu Gln Leu Lys Asp Arg Gln Ser  
65 70 75 80

Gly Asp Asp Glu Ala Met Ala Leu Asp Glu Thr Phe Cys Thr Ala Leu  
85 90 95

Glu Tyr Gly Leu Pro Pro Thr Gly Gly Trp Gly Leu Gly Ile Asp Arg  
100 105 110

Leu Thr Met Met Leu Thr Asp Ser Gln Asn Ile Lys Glu Val Leu Leu  
115 120 125

Phe Pro Ala Met Lys Pro Gln Glu  
130 135

<210> 17

<211> 1430

<212> DNA

<213> Zea mays

<400> 17

cgaaccgctc gctgctggct cctccgcgcg cgtgtcgcg gcatggccac gcttccaatg 60  
gcgcgtctccc ccgcggccat ttcccccttc accacccctcc ccctctacta ttcttcgcgt 120  
cctcaccgcc gcctccctgc ccgcgttcttc tccgtcgctt cggcacccggg cggagcgaaa 180  
gggcaccgac cggcgccctc cgccgttgag gtggggggcg tcaagatcgcc ggcgcaggat 240  
gttgtgaagg aggatgtacc gacaaacaac gtgcccgaca atatctttc gaagatcgcc 300  
ctgcagctgc acaggaggga taaccatccc cttgggattt tgaagaacac aatttatgat 360  
tactttgaca agaacttcac tggcagttt gacaagttt atgacccctt ccctcttgcgtt 420  
tctgtcaagc agaattttga ttagtgccttgc accatgttaag ccggagttac 480  
aacgacacat attatgtta tggtcaaaca gtcctaaggt gtcataccag tgctcatcaa 540  
gctgagctgc taaggcatgg acatacacac tttcttgtaa ctggagatgt ttaccgtagg 600  
gattccatttgc attcaactca ctatcctgtc ttccatcaga tggaaagggtt ccgtgtcttc 660  
tctcctgtatg aatggtcagg gtctcgcatg ggtggacag catatgcagc tgcagaactc 720  
aagaaaacac tggaaaggctt ggcaagacat ctatgggtt ctgttagagat gcgatgggtt 780  
gacacttact tccccattttac caaccatcc tttgagctcg aaataatactt tcaggatgat 840  
tgggtggagg ttttgggtt tggagtccacc gagcaggaaa ttttggaaaag aaatggcagg 900  
aggaccatg tggcatgggc ctttggattt ggcttggagc gccttgcaat ggtccttttc 960  
gacattccag atattcgact attctggtcg aatgataaac ggttcacgtc ccagttctca 1020  
gaaggcaagc ttgggtgtcaa gttcaagcca ttttcaaagt ttccctcctt ttacaaggat 1080  
atgagtttct ggatcaatga tgcatttaca gaaaacaact tatgtgaggt tgtcagagga 1140  
attgctggtg atcttggtaa ggaggtaaaa cttattgata atttcacgaa caagaaaggc 1200  
atgacgagcc attgctatag aatagcctat aggtcgatgg aacgctcgct cacagacgag 1260  
gagattaaca atcttcagtt gaatgtcagg gaagctgtga aagataaaatt ggaagtagag 1320  
tttagataga agcagcttagc tatgcagttt taccatgaac taaatttgc ctctctttat 1380  
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<210> 18

<211> 442

<212> PRT

<213> Zea mays

<400> 18

Arg Thr Ala Arg Cys Trp Leu Leu Arg Ala Arg Val Arg Gly Met Ala  
1 5 10 15

Thr Leu Pro Met Ala Leu Ser Pro Ala Ala Ile Ser Pro Phe Thr Thr  
20 25 30

Leu Pro Leu Tyr Tyr Ser Ser Arg Pro His Arg Arg Leu Leu Ala Arg  
35 40 45

Phe Phe Ser Val Ala Ser Ala Pro Gly Gly Ala Lys Gly His Arg Pro  
50 55 60

Ala Ala Ser Ala Val Glu Val Gly Gly Val Lys Ile Ala Arg Glu Asp  
 65 70 75 80  
 Val Val Lys Glu Asp Asp Pro Thr Asn Asn Val Pro Asp Asn Ile Phe  
 85 90 95  
 Ser Lys Ile Gly Leu Gln Leu His Arg Arg Asp Asn His Pro Leu Gly  
 100 105 110  
 Ile Leu Lys Asn Thr Ile Tyr Asp Tyr Phe Asp Lys Asn Phe Thr Gly  
 115 120 125  
 Gln Phe Asp Lys Phe Asp Asp Leu Cys Pro Leu Val Ser Val Lys Gln  
 130 135 140  
 Asn Phe Asp Asp Val Leu Val Pro Ser Asp His Val Ser Arg Ser Tyr  
 145 150 155 160  
 Asn Asp Thr Tyr Tyr Val Asp Gly Gln Thr Val Leu Arg Cys His Thr  
 165 170 175  
 Ser Ala His Gln Ala Glu Leu Leu Arg His Gly His Thr His Phe Leu  
 180 185 190  
 Val Thr Gly Asp Val Tyr Arg Arg Asp Ser Ile Asp Ser Thr His Tyr  
 195 200 205  
 Pro Val Phe His Gln Met Glu Gly Phe Arg Val Phe Ser Pro Asp Glu  
 210 215 220  
 Trp Ser Gly Ser Arg Met Gly Gly Thr Ala Tyr Ala Ala Ala Glu Leu  
 225 230 235 240  
 Lys Lys Thr Leu Glu Gly Leu Ala Arg His Leu Phe Gly Ala Val Glu  
 245 250 255  
 Met Arg Trp Val Asp Thr Tyr Phe Pro Phe Thr Asn Pro Ser Phe Glu  
 260 265 270  
 Leu Glu Ile Tyr Phe Gln Asp Asp Trp Leu Glu Val Leu Gly Cys Gly  
 275 280 285  
 Val Thr Glu Gln Glu Ile Leu Lys Arg Asn Gly Arg Arg Asp His Val  
 290 295 300  
 Ala Trp Ala Phe Gly Leu Gly Leu Glu Arg Leu Ala Met Val Leu Phe  
 305 310 315 320  
 Asp Ile Pro Asp Ile Arg Leu Phe Trp Ser Asn Asp Lys Arg Phe Thr  
 325 330 335  
 Ser Gln Phe Ser Glu Gly Lys Leu Gly Val Lys Phe Lys Pro Phe Ser  
 340 345 350  
 Lys Phe Pro Pro Cys Tyr Lys Asp Met Ser Phe Trp Ile Asn Asp Ala  
 355 360 365  
 Phe Thr Glu Asn Asn Leu Cys Glu Val Val Arg Gly Ile Ala Gly Asp  
 370 375 380

Leu Val Glu Glu Val Lys Leu Ile Asp Asn Phe Thr Asn Lys Lys Gly  
385 390 395 400

Met Thr Ser His Cys Tyr Arg Ile Ala Tyr Arg Ser Met Glu Arg Ser  
405 410 415

Leu Thr Asp Glu Glu Ile Asn Asn Leu Gln Leu Asn Val Arg Glu Ala  
420 425 430

Val Lys Asp Lys Leu Glu Val Glu Leu Arg  
435 440

<210> 19

<211> 1000

<212> DNA

<213> Oryza sativa

<400> 19

gcacgagtgg taccaacacgc atccctgctcg ggattcacac gatacatttt ttcttgaagc 60  
ccctgccgtt acaaaacaat tgcctgaaga ttatcttgag aaagtaaagg aagttcatca 120  
acgtgggtgt tatggctcca agggatatgg ctatgactgg aaacgggatg aagcagagaa 180  
aaacctgctt cgtaccacaca ctacagcagt ttcaacaagg atgctataca agctagcaca 240  
agagaaacct tttgccccta agaggtacta ctccattgtat cgtgtttcc gcaatgaagc 300  
tgtggaccgg actcatcttg cggaattcca ccagattgaa ggtctcattt gtgattatgg 360  
tttgacgctg ggtgatctga ttgggtgtatt ggaggatttc ttctcgagtc taggcatgtc 420  
aaagctgcgt ttcaaggctg cctacaatcc atacaccgag ccgagcatgg aaattttcag 480  
ttaccatgaa ggtttaaaga aatgggtgaa agttggtaac tctggcatgt tcagacctga 540  
aatgttactt cccatgggac tgccagaggg tgttaatgtt attgcatggg gtctttca 600  
agaaaggcca acaatgattc tttacggcat cgacaacatt cgagacctct ttggaccaaa 660  
ggttgatttc aacctcatca agagcaaccc tctctgccgc ttggactgc agtaaaacct 720  
tgcaaaagtt ggttggaaat gattaagtaa caagatttgtt tagttgatc agtgggtgaa 780  
cgtgaagaga tcatttctgg cttaccttga aacaccaata catgtgcatt tagcagaggt 840  
ttttgttata cagtttgag tgatatgaga ctaccagcca atttttgtt gtgtccatat 900  
tcgaataactt tgatacattt taattgagca catccaatgt atgaagtgg catctgcccgc 960  
tgcgggtgct tgaatcaaaa aaaaaaaaaa aaaaaaaaaa 1000

<210> 20

<211> 237

<212> PRT

<213> Oryza sativa

<400> 20

His Glu Trp Tyr Gln Gln His Pro Ala Arg Asp Ser His Asp Thr Phe  
1 5 10 15

Phe Leu Glu Ala Pro Ala Ala Thr Lys Gln Leu Pro Glu Asp Tyr Leu  
20 25 30

Glu Lys Val Lys Glu Val His Gln Arg Gly Gly Tyr Gly Ser Lys Gly  
35 40 45

Tyr Gly Tyr Asp Trp Lys Arg Asp Glu Ala Glu Lys Asn Leu Leu Arg  
50 55 60

Thr His Thr Thr Ala Val Ser Thr Arg Met Leu Tyr Lys Leu Ala Gln  
65 70 75 80

Glu Lys Pro Phe Ala Pro Lys Arg Tyr Tyr Ser Ile Asp Arg Val Phe  
85 90 95

Arg Asn Glu Ala Val Asp Arg Thr His Leu Ala Glu Phe His Gln Ile  
100 105 110

Glu Gly Leu Ile Cys Asp Tyr Gly Leu Thr Leu Gly Asp Leu Ile Gly  
115 120 125

Val Leu Glu Asp Phe Phe Ser Ser Leu Gly Met Ser Lys Leu Arg Phe  
130 135 140

Lys Pro Ala Tyr Asn Pro Tyr Thr Glu Pro Ser Met Glu Ile Phe Ser  
145 150 155 160

Tyr His Glu Gly Leu Lys Lys Trp Val Glu Val Gly Asn Ser Gly Met  
165 170 175

Phe Arg Pro Glu Met Leu Leu Pro Met Gly Leu Pro Glu Gly Val Asn  
180 185 190

Val Ile Ala Trp Gly Leu Ser Leu Glu Arg Pro Thr Met Ile Leu Tyr  
195 200 205

Gly Ile Asp Asn Ile Arg Asp Leu Phe Gly Pro Lys Val Asp Phe Asn  
210 215 220

Leu Ile Lys Ser Asn Pro Leu Cys Arg Leu Gly Leu Gln  
225 230 235

<210> 21  
<211> 387  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (337)

<220>  
<221> unsure  
<222> (379)

<400> 21  
gattgc当地 ggatcatgga aagaaaaatc attcaaatact ttgaatttag gaaaaggagt 60  
catgggtgtc cctccaaatg gtggccatct tcacacttta cttaaatgca gaactatgat 120  
gaaagaaaatc ttcttgaaaa tgggatttga agaaatgcc accaacaatt acgttgaatc 180  
ttctttctgg aattttgata ctttatttca acctcaacaa catcctgctc gtgatgctca 240  
cgatactttc ttcccttctg aacctgcata tgccaaatcc attccacaag attatttaga 300  
aagagtgaaa acaatgcata agaaaaggagg gcacggntct attgggtgga gatacgactg 360  
gagtggaaac tgagtccana aaaaaaa 387

<210> 22  
<211> 123  
<212> PRT  
<213> Glycine max

<400> 22  
Ile Ala Asn Gly Ser Trp Lys Glu Lys Ser Phe Lys Ser Leu Asn Leu  
1 5 10 15

Gly Lys Gly Val Met Gly Val Pro Pro Asn Gly Gly His Leu His Thr  
20 25 30

Leu Leu Lys Cys Arg Thr Met Met Lys Glu Ile Phe Leu Glu Met Gly  
35 40 45

Phe Glu Glu Met Pro Thr Asn Asn Tyr Val Glu Ser Ser Phe Trp Asn  
50 55 60

Phe Asp Thr Leu Phe Gln Pro Gln Gln His Pro Ala Arg Asp Ala His  
65 70 75 80

Asp Thr Phe Phe Leu Ser Glu Pro Ala Ser Ala Lys Ser Ile Pro Gln  
85 90 95

Asp Tyr Leu Glu Arg Val Lys Thr Met His Glu Lys Gly Gly His Gly  
100 105 110

Ser Ile Gly Trp Arg Tyr Asp Trp Ser Gly Asn  
115 120

<210> 23

<211> 1074

<212> DNA

<213> Triticum aestivum

<400> 23

gcacgaggga caaacctattt cgataggata tagccaaccg ttgttagagg tccgtgaggc 60  
aatccagaac atttttctcg agatggggtt cagttagatg ccaacgaaca tgtatgtaga 120  
gagcagcttc tgaaattttt atgcactgtt ccagccacaa cagcatcctg ctcgtgattc 180  
acacgatacc tttttcctca aagcccctgc tacaacaaca caattacctg atgactatct 240  
tgagaaagta aagcaagtac atcagtcgtt tggtcatggc tccaaaggat atggttacga 300  
ttgaaagcga gatgaagcag agaaaaaacct gcttcgtact cacacaactg cagtttcaac 360  
aagatgcta tacaagctag cacaggagaa aacttttgc cctaagagat actattctat 420  
tgatcgtgtt ttccggatg aagctgttgc ccgaactcat ctgcagaat tccaccagat 480  
agaaggctt atttgttgcattt atggtttgc gcttgggtat ctgataggtt tattggagga 540  
tttcttctcc agactaggca tgtcaaagct gcgtttcaaa cctgcctaca acccgatcac 600  
tgaaccaagc atggaaattt tcagctacca cgatggctg aagaaaatggg tggaaatagg 660  
caactcaggc atgttcaggc cgaaaatgtt acttccatg ggactgccag aggggtttaa 720  
tgttatcgca tggggctttt cgcttggaaag gccaaacatg attctgtatg ggattgacaa 780  
catacgttat ctctttggc caaaggctca cttcaatctg atcaagagca gccccatttg 840  
ccgcttgggg ctgttagtgc gtgagcttgc tagaacttta tctggatgtc tggatgcgaa 900  
ggatgtttat ttgtggttat acctttgaaa accagttactt gtgcatttaa cagaggagtt 960  
gcagaaatac acacatgttag ctctgaattt caaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1020  
aataaaaaaaaaaa aaacaaaaaaaaaa aaaaaaaaaaa tactcgaggg gggccgtac caca 1074

<210> 24

<211> 284

<212> PRT

<213> Triticum aestivum

<400> 24

His Glu Gly Gln Pro Ile Ala Ile Gly Tyr Ser Gln Pro Leu Leu Glu  
1 5 10 15

Val Arg Glu Ala Ile Gln Asn Ile Phe Leu Glu Met Gly Phe Ser Glu  
20 25 30

Met Pro Thr Asn Met Tyr Val Glu Ser Ser Phe Trp Asn Phe Asp Ala  
35 40 45

Leu Phe Gln Pro Gln Gln His Pro Ala Arg Asp Ser His Asp Thr Phe  
50 55 60

Phe Leu Lys Ala Pro Ala Thr Thr Thr Gln Leu Pro Asp Asp Tyr Leu  
65 70 75 80

Glu Lys Val Lys Gln Val His Gln Ser Gly Gly His Gly Ser Lys Gly  
85 90 95

Tyr Gly Tyr Asp Trp Lys Arg Asp Glu Ala Glu Lys Asn Leu Leu Arg  
100 105 110

Thr His Thr Thr Ala Val Ser Thr Arg Met Leu Tyr Lys Leu Ala Gln  
115 120 125

Glu Lys Thr Phe Ala Pro Lys Arg Tyr Tyr Ser Ile Asp Arg Val Phe  
130 135 140

Arg Asn Glu Ala Val Asp Arg Thr His Leu Ala Glu Phe His Gln Ile  
145 150 155 160

Glu Gly Leu Ile Cys Asp Tyr Gly Leu Thr Leu Gly Asp Leu Ile Gly  
165 170 175

Val Leu Glu Asp Phe Phe Ser Arg Leu Gly Met Ser Lys Leu Arg Phe  
180 185 190

Lys Pro Ala Tyr Asn Pro Tyr Thr Glu Pro Ser Met Glu Ile Phe Ser  
195 200 205

Tyr His Asp Gly Leu Lys Trp Val Glu Ile Gly Asn Ser Gly Met  
210 215 220

Phe Arg Pro Glu Met Leu Leu Pro Met Gly Leu Pro Glu Gly Val Asn  
225 230 235 240

Val Ile Ala Trp Gly Leu Ser Leu Glu Arg Pro Thr Met Ile Leu Tyr  
245 250 255

Gly Ile Asp Asn Ile Arg Asp Leu Phe Gly Pro Lys Val Asp Phe Asn  
260 265 270

Leu Ile Lys Ser Ser Pro Ile Cys Arg Leu Gly Leu  
275 280

<210> 25

<211> 1939

<212> DNA

<213> Zea mays

<400> 25

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ctctgactcg agtggccgct actctacccc acccacaccc ttccgccccgc cgccactaaa 120  
ccctagcggg acacccgcct tgctcgcgcc gcctcatcct ctcactcctc tcggacccccc 180  
ggtgcccggt gcagagctgc gcgaccgaga accgaatctg tgagccatgt cgaccaacaa 240  
ggcagcgcg gccaaggcg gcccgggaa gaagaaggag gtgaagaagg agacgaagct 300  
cggatggcc tataagaagg acgacaactt cggggagtgg tactccgagg ttgttgtaa 360  
cagtgaaatg attgagact atgacatttc tggttgat atattgaggc catggcgt 420  
ggaaatctgg gagctactga aagaattctt tgatgcagaa attaaaaagc tgaagctcaa 480  
accatattat ttccctttgt ttgttactga gaatgttcta cagaaggaaa aggaccacat 540

tgagggctt gcacctgagg tagctgggt tactaaatct gggaaatctg acctggaagc 600  
 accgattgca atccgc(cc)ca caagttagac tgtcatgtat ccgtacttct ccaaatggat 660  
 aagaagccac cgagacttac ctttgagggtg taatcaatgg tgtaatgttg ttagatggga 720  
 gtttagcaat ccaactccct tcataaggag ccgtgaattt ctgtggcaag aggggcatac 780  
 tgctttgcg actaaagaag aggcatgtga agaggttctc caaatattgg aactgtaccg 840  
 aaggatatac gaagaatttt tagcagttcc agtttccaaa gggagaaaaa gcgagatgga 900  
 aaaatttgca ggtggcctt ataccaccag cgttgaggcc ttcatccaa acactggtcg 960  
 tggcatacaa ggcgcaacct cacactgtct tggtaaaaac ttgccaaga tgtttgat 1020  
 cactttgag aatgagaaag gtgttaggaa aatggtttg caaaacttctt gggcttacac 1080  
 aaccgcctcg attggagtga tggatgtac acatgtgtat gacaaggct tagtattacc 1140  
 accaaagggtg gcaccaatcc agtaatcgt gatttcatgt cttataagg acgctgacac 1200  
 aactgccata aagggagcct gcaaatcaac tgtttacaca ctcgtacat ctgggattag 1260  
 agcggatcag gacaccgtg aaaattactc tccagttgg aagtattccc actggaaat 1320  
 gaaagggttt ccattgagaa ttgagattgg tccaaaagat ctggcaaaca aacaggtgcg 1380  
 tggatgtccgc cgggacaacg gtgcaaaaggt tgacatccct gtgaccaatt tggttgaaga 1440  
 ggttaaagtg ttactggatg agattcaaaa aaatctgttc aaaacagccc aagaaaagag 1500  
 agatgcctgt gttcatgtcg tgaacacttg ggatgaattc acaactgctc tgaataacaa 1560  
 aaagttgatc ttggctccat ggtgtatga ggaggaaatt gagaagatg taaaaactcg 1620  
 gacaaaaggg gaacttggag ctgcggaaac attgtgtact ccatttgagc agccagaact 1680  
 tccagaaggt accctgtgct ttgatctgg aaagccagcg aagaagtggt cggtctgggg 1740  
 cccgagctac tgattgcctg tgctgggatt atttctggat tcaatcttag tgagttatgt 1800  
 agctttgaag tgcggatac aaatccaaaaa atccattac attgcgtttt acatcgactt 1860  
 gcagttctca tgcataact gctgacaaaaa gccatcgatt tcctgtggac catgctattc 1920  
 gagttgaat gttgcaagg 1939

<210> 26

<211> 383

<212> PRT

<213> Zea mays

<400> 26

Pro	Ile	Ala	Ile	Arg	Pro	Thr	Ser	Glu	Thr	Val	Met	Tyr	Pro	Tyr	Phe
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Ser	Lys	Trp	Ile	Arg	Ser	His	Arg	Asp	Leu	Pro	Leu	Arg	Cys	Asn	Gln
			20					25				30			

Trp	Cys	Asn	Val	Val	Arg	Trp	Glu	Phe	Ser	Asn	Pro	Thr	Pro	Phe	Ile
			35			40					45				

Arg	Ser	Arg	Glu	Phe	Leu	Trp	Gln	Glu	Gly	His	Thr	Ala	Phe	Ala	Thr
			50			55				60					

Lys	Glu	Glu	Ala	Asp	Glu	Glu	Val	Leu	Gln	Ile	Leu	Glu	Leu	Tyr	Arg
			65			70			75			80			

Arg	Ile	Tyr	Glu	Glu	Phe	Leu	Ala	Val	Pro	Val	Ser	Lys	Gly	Arg	Lys
			85			90				95					

Ser	Glu	Met	Glu	Lys	Phe	Ala	Gly	Gly	Leu	Tyr	Thr	Ser	Val	Glu
			100					105			110			

Ala	Phe	Ile	Pro	Asn	Thr	Gly	Arg	Gly	Ile	Gln	Gly	Ala	Thr	Ser	His
			115			120			125						

Cys	Leu	Gly	Gln	Asn	Phe	Ala	Lys	Met	Phe	Asp	Ile	Thr	Phe	Glu	Asn
			130			135			140						

Glu	Lys	Gly	Val	Arg	Glu	Met	Val	Trp	Gln	Asn	Ser	Trp	Ala	Tyr	Thr
			145			150			155			160			

Thr Arg Ser Ile Gly Val Met Val Met Thr His Gly Asp Asp Lys Gly  
 165 170 175  
 Leu Val Leu Pro Pro Lys Val Ala Pro Ile Gln Val Ile Val Ile Ser  
 180 185 190  
 Val Pro Tyr Lys Asp Ala Asp Thr Thr Ala Ile Lys Gly Ala Cys Glu  
 195 200 205  
 Ser Thr Val Tyr Thr Leu Asp Gln Ser Gly Ile Arg Ala Asp Gln Asp  
 210 215 220  
 Thr Arg Glu Asn Tyr Ser Pro Gly Trp Lys Tyr Ser His Trp Glu Met  
 225 230 235 240  
 Lys Gly Val Pro Leu Arg Ile Glu Ile Gly Pro Lys Asp Leu Ala Asn  
 245 250 255  
 Lys Gln Val Arg Val Val Arg Arg Asp Asn Gly Ala Lys Val Asp Ile  
 260 265 270  
 Pro Val Thr Asn Leu Val Glu Glu Val Lys Val Leu Leu Asp Glu Ile  
 275 280 285  
 Gln Lys Asn Leu Phe Lys Thr Ala Gln Glu Lys Arg Asp Ala Cys Val  
 290 295 300  
 His Val Val Asn Thr Trp Asp Glu Phe Thr Thr Ala Leu Asn Asn Lys  
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 Lys Leu Ile Leu Ala Pro Trp Cys Asp Glu Glu Glu Ile Glu Lys Asp  
 325 330 335  
 Val Lys Thr Arg Thr Lys Gly Glu Leu Gly Ala Ala Lys Thr Leu Cys  
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 gttattgtga ttccctgtgcc ttacaaaagat gccgataactc aaggaatctt tgatgcctgt 600  
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Phe Ser Asn Pro Thr Pro Xaa Ile Arg Ser Arg Glu Phe Leu Trp Gln  
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Glu Gly His Thr Ala Phe Ala Thr Lys Asp Glu Ala Xaa Ala Glu Val  
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Leu Glu Ile Leu Glu Leu Tyr Arg Arg Ile Tyr Glu Glu Tyr Leu Ala  
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Val Pro Val Ile Lys Gly Lys Xaa Ser Glu Leu Glu Lys Phe Ala Gly  
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Gly Leu Tyr Thr Xaa Asn Val Glu Ala Phe Ile Pro Asn Thr Gly Arg  
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Gly Ile Gln Gly Ala Thr Ser His Cys Leu Gly Gln Asn Phe Ala Lys  
115 120 125

Met Phe Glu Ile Asn Phe Glu Asn Glu Lys Gly Glu Lys Ala Met Val  
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 aatatatgaa gaatttttag cagttccagt gtccaaaggg agaaaaagtg agatgaaaa 180  
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Pro Val Ser Lys Gly Arg Lys Ser Glu Met Glu Lys Phe Ala Gly Gly  
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Leu Tyr Thr Thr Ser Val Glu Ala Phe Ile Pro Asn Thr Gly Arg Gly  
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Ile Gln Gly Ala Thr Ser His Cys Leu Gly Gln Asn Phe Ala Lys Met  
 85 90 95

Phe Asp Ile Thr Phe Glu Asn Glu Lys Gly Glu Arg Ser Met Val Trp  
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Gln Asn Ser Trp Ala Tyr Thr Thr Arg Ser Ile Gly Val Met Ile Met  
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 Pro Gly His Cys Ile Leu Cys His  
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 35 40 45  
 Ala Thr Gly Thr Pro His Tyr Gly His Ile Leu Ala Ser Thr Ile Lys  
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 Asp Ile Val Pro Arg Tyr Ala Thr Met Thr Gly His His Val Glu Arg  
 65 70 75 80  
 Arg Phe Gly Trp Asp Thr His Gly Val Pro Ile Glu His Ile Ile Asp  
 85 90 95  
 Lys Lys Leu Gly Ile Thr Gly Lys Asp Asp Val Phe Lys Tyr Gly Leu  
 100 105 110  
 Glu Asn Tyr Asn Asn Glu Cys Arg Ser Ile Val Met Thr Tyr Ala Ser  
 115 120 125  
 Asp Trp Arg Lys Thr Ile Gly Arg Leu Gly Arg Trp Ile Asp Phe Asp  
 130 135 140  
 Asn Asp Tyr Lys Thr Met Tyr Pro Ser Phe Met Glu Ser Thr Trp Trp  
 145 150 155 160  
 Ala Phe Lys Gln Leu His Glu Lys Gly Gln Val Tyr Arg Gly Phe Lys  
 165 170 175  
 Val Met Pro Tyr Ser Thr Gly Leu Thr Thr Pro Leu Ser Asn Phe Glu  
 180 185 190  
 Ala Gln Gln Asn Tyr Lys Asp Val Asn Asp Pro Ala Val Thr Ile Gly  
 195 200 205  
 Phe Asn Val Ile Gly Gln Glu Lys Thr Gln Leu Val Ala Trp Thr Thr  
 210 215 220  
 Thr Pro Trp Thr Leu Pro Ser Asn Leu Ser Leu Cys Val Asn Ala Asp  
 225 230 235 240

Phe Glu Tyr Val Lys Ile Tyr Asp Glu Thr Arg Asp Arg Tyr Phe Ile  
 245 250 255  
 Leu Leu Glu Ser Leu Ile Lys Thr Leu Tyr Lys Lys Pro Lys Asn Glu  
 260 265 270  
 Lys Tyr Lys Ile Val Glu Lys Ile Lys Gly Ser Asp Leu Val Gly Leu  
 275 280 285  
 Lys Tyr Glu Pro Leu Phe Pro Tyr Phe Ala Glu Gln Phe His Glu Thr  
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 Ala Phe Arg Val Ile Ser Asp Asp Tyr Val Thr Ser Asp Ser Gly Thr  
 305 310 315 320  
 Gly Ile Val His Asn Ala Pro Ala Phe Gly Glu Asp Asn Ala Ala  
 325 330 335  
 Cys Leu Lys Asn Gly Val Ile Ser Glu Asp Ser Val Leu Pro Asn Ala  
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 Ile Asp Asp Leu Gly Arg Phe Thr Lys Asp Val Pro Asp Phe Glu Gly  
 355 360 365  
 Val Tyr Val Lys Asp Ala Asp Lys Leu Ile Ile Lys Tyr Leu Thr Asn  
 370 375 380  
 Thr Gly Asn Leu Leu Leu Ala Ser Gln Ile Arg His Ser Tyr Pro Phe  
 385 390 395 400  
 Cys Trp Arg Ser Asp Thr Pro Leu Leu Tyr Arg Ser Val Pro Ala Trp  
 405 410 415  
 Phe Val Arg Val Lys Asn Ile Val Pro Gln Met Leu Asp Ser Val Met  
 420 425 430  
 Lys Ser His Trp Val Pro Asn Thr Ile Lys Glu Lys Arg Phe Ala Asn  
 435 440 445  
 Trp Ile Ala Asn Ala Arg Asp Trp Asn Val Ser Arg Asn Arg Tyr Trp  
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 Gly Thr Pro Ile Pro Leu Trp Val Ser Asp Asp Phe Glu Glu Val Val  
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 Cys Val Gly Ser Ile Lys Glu Leu Glu Glu Leu Thr Gly Val Arg Asn  
 485 490 495  
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 Glu Asn Thr Glu Lys Phe Asp Glu Arg Val Pro Ala Asn Phe Ile Ser  
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Glu Gly Leu Asp Gln Thr Arg Gly Trp Phe Tyr Thr Leu Ala Val Leu  
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 Gly Thr His Leu Phe Gly Ser Val Pro Tyr Lys Asn Val Ile Val Ser  
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 Gly Ile Val Leu Ala Ala Asp Gly Arg Lys Met Ser Lys Ser Leu Lys  
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 Leu Arg Leu Tyr Leu Ile Asn Ser Pro Val Leu Lys Ala Glu Ser Leu  
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 Lys Phe Lys Glu Glu Gly Val Lys Glu Val Val Ser Lys Val Leu Leu  
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 Pro Trp Trp Asn Ser Phe Lys Phe Leu Asp Gly Gln Ile Ala Leu Leu  
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 Lys Lys Met Ser Asn Ile Asp Phe Gln Tyr Asp Asp Ser Val Lys Ser  
 675 680 685  
 Asp Asn Val Met Asp Arg Trp Ile Leu Ala Ser Met Gln Ser Leu Val  
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 Pro Lys Leu Leu Asn Phe Ile Asp Glu Leu Thr Asn Trp Tyr Ile Arg  
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 Phe Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Val Glu Asp Cys Leu  
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 Lys Ala Leu Asn Ser Leu Phe Asp Ala Leu Phe Thr Phe Val Arg Ala  
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 Met Ala Pro Phe Thr Pro Phe Leu Ser Glu Ser Ile Tyr Leu Arg Leu  
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 Lys Glu Tyr Ile Pro Glu Ala Val Leu Ala Lys Tyr Gly Lys Asp Gly  
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 Arg Ser Val His Phe Leu Ser Tyr Pro Val Val Lys Lys Glu Tyr Phe  
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 Asp Glu Ala Ile Glu Thr Ala Val Ser Arg Met Gln Ser Val Ile Asp  
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 Leu Lys Thr Leu Val Ile Leu His Ser Asp Glu Ser Tyr Leu Lys Asp  
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 Val Glu Ala Leu Lys Asn Tyr Ile Ile Glu Glu Leu Asn Val Arg Asp  
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Val Val Ile Thr Ser Asp Glu Ala Lys Tyr Gly Val Glu Tyr Lys Ala  
                   885                     890                     895  
  
 Val Ala Asp Trp Pro Val Leu Gly Lys Lys Leu Lys Lys Asp Ala Lys  
                   900                     905                     910  
  
 Lys Val Lys Asp Ala Leu Pro Ser Val Thr Ser Glu Gln Val Arg Glu  
                   915                     920                     925  
  
 Tyr Leu Glu Ser Gly Lys Leu Glu Val Ala Gly Ile Glu Leu Val Lys  
                   930                     935                     940  
  
 Gly Asp Leu Asn Ala Ile Arg Gly Leu Pro Glu Ser Ala Val Gln Ala  
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 Gly Gln Glu Thr Arg Thr Asp Gln Asp Val Leu Ile Ile Met Asp Thr  
                   965                     970                     975  
  
 Asn Ile Tyr Ser Glu Leu Lys Ser Glu Gly Leu Ala Arg Glu Leu Val  
                   980                     985                     990  
  
 Asn Arg Ile Gln Lys Leu Arg Lys Lys Cys Gly Leu Glu Ala Thr Asp  
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Glu Tyr Glu Ile Asp Lys Thr Leu Gly Ile Arg Gly Pro Glu Asp Val  
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 Met Arg Tyr Ser Ala Glu Trp Lys Ser Thr Val Ser Arg Leu Gly Arg  
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 Glu Ser Val Trp Trp Val Phe Lys Gln Leu Tyr Asp Lys Gly Leu Val  
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 Tyr Arg Gly Val Lys Val Met Pro Phe Ser Thr Ala Cys Asn Thr Pro  
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 Leu Ser Asn Phe Glu Ser His Gln Asn Tyr Lys Asp Val Gln Asp Pro  
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 Gly Arg Leu Leu Ile Leu Met Glu Ala Arg Leu Ser Ala Leu Tyr Lys  
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 Leu Glu Ser Asp Tyr Glu Ile Leu Glu Arg Phe Pro Gly Ala Tyr Leu  
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 Lys Gly Lys Lys Tyr Arg Pro Leu Phe Asp Tyr Phe Leu Lys Cys Lys  
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 Tyr Arg Val Cys Met Asp Phe Asn Ile Ile Arg Lys Asp Ser Leu Pro  
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 370 375 380  
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 Tyr Pro Phe Cys Trp Arg Ser Asp Thr Pro Leu Ile Tyr Lys Ala Val  
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Pro Ser Trp Phe Val Arg Val Glu Asn Met Val Asp Gln Leu Leu Arg  
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 Val Asn Gly Leu Val Leu Ala Ser Asp Gly Gln Lys Met Ser Lys Arg  
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 Leu Leu Pro Trp Tyr Asn Ala Tyr Arg Phe Leu Ile Gln Asn Val Leu  
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 Arg Leu Gln Lys Glu Glu Ile Glu Phe Leu Tyr Asn Glu Asn Thr  
 675 680 685  
 Val Arg Glu Ser Pro Asn Ile Thr Asp Arg Trp Ile Leu Ser Phe Met  
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Trp Tyr Val Arg Met Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Met  
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 Arg Ala Glu Pro Asp His Met Val Leu Gly Lys Arg Leu Lys Gly Ala  
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 Gly Lys Thr Leu Cys Val Thr Ala Gly Ser Ala Pro Ser Leu Ile Asn  
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 Lys Gln Ser Lys His Lys Pro Lys Phe Thr Phe Tyr Asp Gly Pro Pro  
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Lys Asp Ile Val Thr Arg Tyr Ala His Gln Ser Gly Phe His Val Asp  
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 Ala Glu Trp Lys Ser Thr Val Ser Arg Leu Gly Arg Trp Ile Asp Phe  
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 Trp Val Phe Lys Gln Leu Tyr Asp Lys Gly Leu Val Tyr Arg Gly Val  
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 Lys Val Met Pro Phe Ser Thr Ala Cys Asn Thr Pro Leu Ser Asn Phe  
 180 185 190  
 Glu Ser His Gln Asn Tyr Lys Asp Val Gln Asp Pro Ser Val Phe Val  
 195 200 205  
 Thr Phe Pro Leu Glu Glu Asp Glu Thr Val Ser Leu Val Ala Trp Thr  
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 Thr Thr Pro Trp Thr Leu Pro Ser Asn Leu Ala Val Cys Val Asn Pro  
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 260 265 270  
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 Tyr Arg Pro Leu Phe Asp Tyr Phe Leu Lys Cys Lys Glu Asn Gly Ala  
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 Val Val His Gln Ala Pro Tyr Phe Gly Ala Glu Asp Tyr Arg Val Cys  
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 340 345 350  
 Asp Ala Ser Gly Cys Phe Thr Thr Glu Val Thr Asp Phe Ala Gly Gln  
 355 360 365  
 Tyr Val Lys Asp Ala Asp Lys Ser Ile Ile Arg Thr Leu Lys Glu Gln  
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Gly Arg Leu Leu Val Ala Thr Thr Phe Thr His Ser Tyr Pro Phe Cys  
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 Cys Tyr Trp Val Pro Glu Leu Val Arg Glu Lys Arg Phe Gly Asn Trp  
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 Gly Lys Gly Ser Leu His Arg Ile Ser Glu Val Phe Asp Cys Trp Phe  
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 Lys Arg Glu Phe Glu Asp Ala Phe Pro Ala Asp Phe Ile Ala Glu Gly  
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 Ala Leu Phe Gly Gln Pro Pro Phe Lys Asn Val Ile Val Asn Gly Leu  
 580 585 590  
 Val Leu Ala Ser Asp Gly Gln Lys Met Ser Lys Arg Lys Lys Asn Tyr  
 595 600 605  
 Pro Asp Pro Val Ser Ile Ile Gln Lys Tyr Gly Ala Asp Ala Leu Arg  
 610 615 620  
 Leu Tyr Leu Ile Asn Ser Pro Val Val Arg Ala Glu Asn Leu Arg Phe  
 625 630 635 640  
 Lys Glu Glu Gly Val Arg Asp Val Leu Lys Asp Val Leu Leu Pro Trp  
 645 650 655  
 Tyr Asn Ala Tyr Arg Phe Leu Ile Gln Asn Val Leu Arg Leu Gln Lys  
 660 665 670  
 Glu Glu Glu Ile Glu Phe Leu Tyr Asn Glu Asn Thr Val Arg Glu Ser  
 675 680 685  
 Pro Asn Ile Thr Asp Arg Trp Ile Leu Ser Phe Met Gln Ser Leu Ile  
 690 695 700

Gly Phe Phe Glu Thr Glu Met Ala Ala Tyr Arg Leu Tyr Thr Val Val  
 705 710 715 720  
 Pro Arg Leu Val Lys Phe Val Asp Ile Leu Thr Asn Trp Tyr Val Arg  
 725 730 735  
 Met Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Met Glu Asp Cys Val  
 740 745 750  
 Met Ala Leu Glu Thr Leu Phe Ser Val Leu Leu Ser Leu Cys Arg Leu  
 755 760 765  
 Ile Ala Pro Tyr Thr Pro Phe Leu Thr Glu Leu Met Tyr Gln Asn Leu  
 770 775 780  
 Lys Val Leu Ile Asp Pro Val Ser Val Gln Asp Lys Asp Thr Leu Ser  
 785 790 795 800  
 Ile His Tyr Leu Met Leu Pro Arg Val Arg Glu Glu Leu Ile Asp Lys  
 805 810 815  
 Lys Thr Glu Ser Ala Val Ser Gln Met Gln Ser Val Ile Glu Leu Gly  
 820 825 830  
 Arg Val Ile Arg Asp Arg Lys Thr Ile Pro Ile Lys Tyr Pro Leu Lys  
 835 840 845  
 Glu Ile Val Val Ile His Gln Asp Pro Glu Ala Leu Lys Asp Ile Lys  
 850 855 860  
 Ser Leu Glu Lys Tyr Ile Ile Glu Glu Leu Asn Val Arg Lys Val Thr  
 865 870 875 880  
 Leu Ser Thr Asp Lys Asn Lys Tyr Gly Ile Arg Leu Arg Ala Glu Pro  
 885 890 895  
 Asp His Met Val Leu Gly Lys Arg Leu Lys Gly Ala Phe Lys Ala Val  
 900 905 910  
 Met Thr Ser Ile Lys Gln Leu Ser Ser Glu Glu Leu Glu Gln Phe Gln  
 915 920 925  
 Lys Thr Gly Thr Ile Val Val Glu Gly His Glu Leu His Asp Glu Asp  
 930 935 940  
 Ile Arg Leu Met Tyr Thr Phe Asp Gln Ala Thr Gly Gly Thr Ala Gln  
 945 950 955 960  
 Phe Glu Ala His Ser Asp Ala Gln Ala Leu Val Leu Leu Asp Val Thr  
 965 970 975  
 Pro Asp Gln Ser Met Val Asp Glu Gly Met Ala Arg Glu Val Ile Asn  
 980 985 990  
 Arg Ile Gln Lys Leu Arg Lys Lys Cys Asn Leu Val Pro Thr Asp Glu  
 995 1000 1005  
 Ile Thr Val Tyr Tyr Lys Ala Lys Ser Glu Gly Thr Tyr Leu Asn Ser  
 1010 1015 1020

Val Ile Glu Ser His Thr Glu Phe Ile Phe Thr Thr Ile Lys Ala Pro  
 1025 1030 1035 1040  
 Leu Lys Pro Tyr Pro Val Ser Pro Ser Asp Lys Val Leu Ile Gln Glu  
 1045 1050 1055  
 Lys Thr Gln Leu Lys Gly Ser Glu Leu Glu Ile Thr Leu Thr Arg Gly  
 1060 1065 1070  
 Ser Ser Leu Pro Gly Pro Ala Cys Ala Tyr Val Asn Leu Asn Ile Cys  
 1075 1080 1085  
 Ala Asn Gly Ser Glu Gln Gly Val Leu Leu Glu Asn Pro Lys  
 1090 1095 1100 1120  
 Gly Asp Asn Arg Leu Asp Leu Leu Lys Leu Lys Ser Val Val Thr Ser  
 1105 1110 1115 1120  
 Ile Phe Gly Val Lys Asn Thr Glu Leu Ala Val Phe His Asp Glu Thr  
 1125 1130 1135  
 Glu Ile Gln Asn Gln Thr Asp Leu Leu Ser Leu Ser Gly Lys Thr Leu  
 1140 1145 1150  
 Cys Val Thr Ala Gly Ser Ala Pro Ser Leu Ile Asn Ser Ser Ser Thr  
 1155 1160 1165  
 Leu Leu Cys Gln Tyr Ile Asn Leu Gln Leu Leu Asn Ala Lys Pro Gln  
 1170 1175 1180  
 Glu Cys Leu Met Gly Thr Val Gly Thr Leu Leu Leu Glu Asn Pro Leu  
 1185 1190 1195 1200  
 Gly Gln Asn Gly Leu Thr His Gln Gly Leu Leu Tyr Glu Ala Ala Lys  
 1205 1210 1215  
 Val Phe Gly Leu Arg Ser Arg Lys Leu Lys Leu Phe Leu Asn Glu Thr  
 1220 1225 1230  
 Gln Thr Gln Glu Ile Thr Glu Asp Ile Pro Val Lys Thr Leu Asn Met  
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 Lys Thr Val Tyr Val Ser Val Leu Pro Thr Thr Ala Asp Phe  
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 Gly Ala Gly Pro Arg Ser Lys Asn Ala Leu Lys Lys Glu Gln Lys Met  
 35 40 45

Lys Gln Lys Glu Glu Glu Lys Arg Arg Lys Asp Glu Glu Lys Ala Glu  
 50 55 60

Lys Ala Lys Gln Ala Pro Lys Ala Ser Ser Gln Lys Ala Val Ala Ala  
 65 70 75 80

Asp Asp Glu Glu Met Asp Ala Thr Gln Tyr Tyr Glu Asn Arg Leu Lys  
 85 90 95

Tyr Leu Ala Ala Glu Lys Ala Lys Gly Glu Asn Pro Tyr Pro His Lys  
 100 105 110

Phe Ala Val Ser Met Ser Ile Pro Lys Tyr Ile Glu Thr Tyr Gly Ser  
 115 120 125

Leu Asn Asn Gly Asp His Val Glu Asn Ala Glu Glu Ser Leu Ala Gly  
 130 135 140

Arg Ile Met Ser Lys Arg Ser Ser Ser Lys Leu Phe Phe Tyr Asp  
 145 150 155 160

Leu His Gly Asp Asp Phe Lys Val Gln Val Met Ala Asp Ala Ser Lys  
 165 170 175

Ser Gly Leu Asp Glu Ala Glu Phe Leu Lys Leu His Ser Asn Ala Lys  
 180 185 190

Arg Gly Asp Ile Val Gly Val Ile Gly Phe Pro Gly Lys Thr Lys Arg  
 195 200 205

Gly Glu Leu Ser Ile Phe Pro Arg Ser Phe Ile Leu Leu Ser His Cys  
 210 215 220

Leu His Met Met Pro Arg Lys Ala Asp Asn Val Asn Ala Lys Lys Pro  
 225 230 235 240

Glu Ile Trp Val Pro Gly Gln Thr Arg Asn Pro Glu Ala Tyr Val Leu  
 245 250 255

Lys Asp Gln Glu Ser Arg Tyr Arg Gln Arg His Leu Asp Met Ile Leu  
 260 265 270

Asn Val Glu Val Arg Gln Ile Phe Arg Thr Arg Ala Lys Ile Ile Ser  
 275 280 285

Tyr Val Arg Arg Phe Leu Asp Asn Lys Asn Phe Leu Glu Val Glu Thr  
 290 295 300

Pro Met Met Asn Met Ile Ala Gly Gly Ala Ala Ala Arg Pro Phe Val  
 305 310 315 320

Thr His His Asn Asp Leu Asp Met Arg Leu Tyr Met Arg Ile Ala Pro  
 325 330 335

Glu Leu Tyr Leu Lys Gln Leu Ile Val Gly Gly Leu Glu Arg Val Tyr  
 340 345 350

Glu Ile Gly Lys Gln Phe Arg Asn Glu Gly Ile Asp Leu Thr His Asn  
 355 360 365

Pro Glu Phe Thr Thr Cys Glu Phe Tyr Met Ala Phe Ala Asp Tyr Asn  
 370 375 380  
 Asp Leu Met Glu Met Thr Glu Val Met Leu Ser Gly Met Val Lys Glu  
 385 390 395 400  
 Leu Thr Gly Gly Tyr Lys Ile Lys Tyr Asn Ala Asn Gly Tyr Asp Lys  
 405 410 415  
 Asp Pro Ile Glu Ile Asp Phe Thr Pro Pro Phe Arg Arg Ile Glu Met  
 420 425 430  
 Ile Gly Glu Leu Glu Lys Val Ala Lys Leu Asn Ile Pro Lys Asp Leu  
 435 440 445  
 Ala Ser Glu Glu Ala Asn Lys Tyr Leu Ile Asp Ala Cys Ala Arg Phe  
 450 455 460  
 Asp Val Lys Cys Pro Pro Gln Thr Thr Ala Arg Leu Leu Asp Lys  
 465 470 475 480  
 Leu Val Gly Glu Phe Leu Glu Pro Thr Cys Val Asn Pro Thr Phe Ile  
 485 490 495  
 Ile Asn Gln Pro Glu Ile Met Ser Pro Leu Ala Lys Trp His Arg Ser  
 500 505 510  
 Lys Ser Gly Leu Thr Glu Arg Phe Glu Leu Phe Ile Asn Lys His Glu  
 515 520 525  
 Leu Cys Asn Ala Tyr Thr Glu Leu Asn Asp Pro Val Val Gln Arg Gln  
 530 535 540  
 Arg Phe Ala Asp Gln Leu Lys Asp Arg Gln Ser Gly Asp Asp Glu Ala  
 545 550 555 560  
 Met Ala Leu Asp Glu Thr Phe Cys Asn Ala Leu Glu Tyr Gly Leu Ala  
 565 570 575  
 Pro Thr Gly Gly Trp Gly Leu Gly Ile Asp Arg Leu Ser Met Leu Leu  
 580 585 590  
 Thr Asp Ser Leu Asn Ile Lys Glu Val Leu Phe Phe Pro Ala Met Arg  
 595 600 605  
 Pro Pro Gln Glu Glu Ser Ala Ala Ala Gln Ala Pro Leu Thr Glu Glu  
 610 615 620  
 Lys Lys  
 625  
 <210> 35  
 <211> 451  
 <212> PRT  
 <213> Homo sapiens  
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Val	Ser	Lys	Ala	Ser	His	Ile	Ser	Arg	Gly	His	Gln	His	Gln	Ala	Trp
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Gly	Ser	Arg	Pro	Pro	Ala	Ala	Glu	Cys	Ala	Thr	Gln	Arg	Ala	Pro	Gly
35							40					45			
Ser	Val	Val	Glu	Leu	Leu	Gly	Lys	Ser	Tyr	Pro	Gln	Asp	Asp	His	Ser
50						55					60				
Asn	Leu	Thr	Arg	Lys	Val	Leu	Thr	Arg	Val	Gly	Arg	Asn	Leu	His	Asn
65					70				75			80			
Gln	Gln	His	His	Pro	Leu	Trp	Leu	Ile	Lys	Glu	Arg	Val	Lys	Glu	His
85							90					95			
Phe	Tyr	Lys	Gln	Tyr	Val	Gly	Arg	Phe	Gly	Thr	Pro	Leu	Phe	Ser	Val
100							105					110			
Tyr	Asp	Asn	Leu	Ser	Pro	Val	Val	Thr	Thr	Trp	Gln	Asn	Phe	Asp	Ser
115							120					125			
Leu	Leu	Ile	Pro	Ala	Asp	His	Pro	Ser	Arg	Lys	Lys	Gly	Asp	Asn	Tyr
130						135				140					
Tyr	Leu	Asn	Arg	Thr	His	Met	Leu	Arg	Ala	His	Thr	Ser	Ala	His	Gln
145					150				155			160			
Trp	Asp	Leu	Leu	His	Ala	Gly	Leu	Asp	Ala	Phe	Leu	Val	Val	Gly	Asp
165							170					175			
Val	Tyr	Arg	Arg	Asp	Gln	Ile	Asp	Ser	Gln	His	Tyr	Pro	Ile	Phe	His
180							185				190				
Gln	Leu	Glu	Ala	Val	Arg	Leu	Phe	Ser	Lys	His	Glu	Leu	Phe	Ala	Gly
195						200				205					
Ile	Lys	Asp	Gly	Glu	Ser	Leu	Gln	Leu	Phe	Glu	Gln	Ser	Ser	Arg	Ser
210						215				220					
Ala	His	Lys	Gln	Glu	Thr	His	Thr	Met	Glu	Ala	Val	Lys	Leu	Val	Glu
225						230			235			240			
Phe	Asp	Leu	Lys	Gln	Thr	Leu	Thr	Arg	Leu	Met	Ala	His	Leu	Phe	Gly
245							250					255			
Asp	Glu	Leu	Glu	Ile	Arg	Trp	Val	Asp	Cys	Tyr	Phe	Pro	Phe	Thr	His
260							265				270				
Pro	Ser	Phe	Glu	Met	Glu	Ile	Asn	Phe	His	Gly	Glu	Trp	Leu	Glu	Val
275							280				285				
Leu	Gly	Cys	Gly	Val	Met	Glu	Gln	Gln	Leu	Val	Asn	Ser	Ala	Gly	Ala
290						295				300					
Gln	Asp	Arg	Ile	Gly	Trp	Ala	Phe	Gly	Leu	Gly	Leu	Glu	Arg	Leu	Ala
305							310			315			320		
Met	Ile	Leu	Tyr	Asp	Ile	Pro	Asp	Ile	Arg	Leu	Phe	Trp	Cys	Glu	Asp
325							330				335				

Glu Arg Phe Leu Lys Gln Phe Cys Val Ser Asn Ile Asn Gln Lys Val  
                  340                 345                 350  
  
 Lys Phe Gln Pro Leu Ser Lys Tyr Pro Ala Val Ile Asn Asp Ile Ser  
                  355                 360                 365  
  
 Phe Trp Leu Pro Ser Glu Asn Tyr Ala Glu Asn Asp Phe Tyr Asp Leu  
                  370                 375                 380  
  
 Val Arg Thr Ile Gly Gly Asp Leu Val Glu Lys Val Asp Leu Ile Asp  
                  385                 390                 395                 400  
  
 Lys Phe Val His Pro Lys Thr His Lys Thr Ser His Cys Tyr Arg Ile  
                  405                 410                 415  
  
 Thr Tyr Arg His Met Glu Arg Thr Leu Ser Gln Arg Glu Val Arg His  
                  420                 425                 430  
  
 Ile His Gln Ala Leu Gln Glu Ala Ala Val Gln Leu Leu Gly Val Glu  
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 Gly Arg Phe  
                  450  
  
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 Glu Ile Lys Ser Thr Leu Ala Thr Phe Pro Gln His Gly Ser Gln Asp  
     20             25                 30  
  
 Val Leu Ser Ala Leu Asn Ser Leu Lys Ala His Asn Lys Leu Glu Phe  
     35             40                 45  
  
 Ser Lys Val Asp Thr Val Thr Tyr Asp Leu Thr Lys Glu Gly Ala Gln  
     50             55                 60  
  
 Ile Leu Asn Glu Gly Ser Tyr Glu Ile Lys Leu Val Lys Leu Ile Gln  
     65             70                 75                 80  
  
 Glu Leu Gly Gln Leu Gln Ile Lys Asp Val Met Ser Lys Leu Gly Pro  
     85             90                 95  
  
 Gln Val Gly Lys Val Gly Gln Ala Arg Ala Phe Lys Asn Gly Trp Ile  
     100            105                 110  
  
 Ala Lys Asn Ala Ser Asn Glu Leu Glu Leu Ser Ala Lys Leu Gln Asn  
     115            120                 125  
  
 Thr Asp Leu Asn Glu Leu Thr Asp Glu Thr Gln Ser Ile Leu Ala Gln  
     130            135                 140  
  
 Ile Lys Asn Asn Ser His Leu Asp Ser Ile Asp Ala Lys Ile Leu Asn  
     145            150                 155                 160

Asp Leu Lys Lys Arg Lys Leu Ile Ala Gln Gly Lys Ile Thr Asp Phe  
 165 170 175  
 Ser Val Thr Lys Gly Pro Glu Phe Ser Thr Asp Leu Thr Lys Leu Glu  
 180 185 190  
 Thr Asp Leu Thr Ser Asp Met Val Ser Thr Asn Ala Tyr Lys Asp Leu  
 195 200 205  
 Lys Phe Lys Pro Tyr Asn Phe Asn Ser Gln Gly Val Gln Ile Ser Ser  
 210 215 220  
 Gly Ala Leu His Pro Leu Asn Lys Val Arg Glu Glu Phe Arg Gln Ile  
 225 230 235 240  
 Phe Phe Ser Met Gly Phe Thr Glu Met Pro Ser Asn Gln Tyr Val Glu  
 245 250 255  
 Thr Gly Phe Trp Asn Phe Asp Ala Leu Tyr Val Pro Gln Gln His Pro  
 260 265 270  
 Ala Arg Asp Leu Gln Asp Thr Phe Tyr Ile Lys Asp Pro Leu Thr Ala  
 275 280 285  
 Glu Leu Pro Asp Asp Lys Thr Tyr Met Asp Asn Ile Lys Ala Val His  
 290 295 300  
 Glu Gln Gly Arg Phe Gly Ser Ile Gly Tyr Arg Tyr Asn Trp Lys Pro  
 305 310 315 320  
 Glu Glu Cys Gln Lys Leu Val Leu Arg Thr His Ser Thr Ala Ile Ser  
 325 330 335  
 Ala Arg Met Leu His Asp Leu Ala Lys Asp Pro Lys Pro Thr Arg Leu  
 340 345 350  
 Phe Ser Ile Asp Arg Val Phe Arg Asn Glu Ala Val Asp Ala Thr His  
 355 360 365  
 Leu Ala Glu Phe His Gln Val Glu Gly Val Leu Ala Asp Tyr Asn Ile  
 370 375 380  
 Thr Leu Gly Asp Leu Ile Lys Phe Met Glu Glu Phe Phe Glu Arg Met  
 385 390 395 400  
 Gly Val Thr Gly Leu Arg Phe Lys Pro Thr Tyr Asn Pro Tyr Thr Glu  
 405 410 415  
 Pro Ser Met Glu Ile Phe Ser Trp His Glu Gly Leu Gln Lys Trp Val  
 420 425 430  
 Glu Ile Gly Asn Ser Gly Met Phe Arg Pro Glu Met Leu Glu Ser Met  
 435 440 445  
 Gly Leu Pro Lys Asp Leu Arg Val Leu Gly Trp Gly Leu Ser Leu Glu  
 450 455 460  
 Arg Pro Thr Met Ile Lys Tyr Lys Val Gln Asn Ile Arg Glu Leu Leu  
 465 470 475 480

Gly His Lys Val Ser Leu Asp Phe Ile Glu Thr Asn Pro Ala Ala Arg  
                         485                                490                        495  
 Leu Asp Glu Asp Leu Tyr Glu  
                         500  
 <210> 37  
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 <213> Homo sapiens  
 <400> 37  
 Met Glu His Thr Glu Ile Asp His Trp Leu Glu Phe Ser Ala Thr Lys  
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 Leu Ser Ser Cys Asp Ser Phe Thr Ser Thr Ile Asn Glu Leu Asn His  
     20                      25                          30  
 Cys Leu Ser Leu Arg Thr Tyr Leu Val Gly Asn Ser Leu Ser Leu Ala  
     35                      40                          45  
 Asp Leu Cys Val Trp Ala Thr Leu Lys Gly Asn Ala Ala Trp Gln Glu  
     50                      55                          60  
 Gln Leu Lys Gln Lys Lys Ala Pro Val His Val Lys Arg Trp Phe Gly  
     65                      70                          75                          80  
 Phe Leu Glu Ala Gln Gln Ala Phe Gln Ser Val Gly Thr Lys Trp Asp  
     85                      90                          95  
 Val Ser Thr Thr Lys Ala Arg Val Ala Pro Glu Lys Lys Gln Asp Val  
     100                    105                          110  
 Gly Lys Phe Val Glu Leu Pro Gly Ala Glu Met Gly Lys Val Thr Val  
     115                    120                          125  
 Arg Phe Pro Pro Glu Ala Ser Gly Tyr Leu His Ile Gly His Ala Lys  
     130                    135                          140  
 Ala Ala Leu Leu Asn Gln His Tyr Gln Val Asn Phe Lys Gly Lys Leu  
     145                    150                          155                          160  
 Ile Met Arg Phe Asp Asp Thr Asn Pro Glu Lys Glu Lys Glu Asp Phe  
     165                    170                          175  
 Glu Lys Val Ile Leu Glu Asp Val Ala Met Leu His Ile Lys Pro Asp  
     180                    185                          190  
 Gln Phe Thr Tyr Thr Ser Asp His Phe Glu Thr Ile Met Lys Tyr Ala  
     195                    200                          205  
 Glu Lys Leu Ile Gln Glu Gly Lys Ala Tyr Val Asp Asp Thr Pro Ala  
     210                    215                          220  
 Glu Gln Met Lys Ala Glu Arg Glu Gln Arg Ile Glu Ser Lys His Arg  
     225                    230                          235                          240  
 Lys Asn Pro Ile Glu Lys Asn Leu Gln Met Trp Glu Glu Met Lys Lys  
     245                    250                          255

Gly Ser Gln Phe Gly His Ser Cys Cys Leu Arg Ala Lys Ile Asp Met  
                  260                 265                 270  
  
 Ser Ser Asn Asn Gly Cys Met Arg Asp Pro Thr Leu Tyr Arg Cys Lys  
                  275                 280                 285  
  
 Ile Gln Pro His Pro Arg Thr Gly Asn Lys Tyr Asn Val Tyr Pro Thr  
                  290                 295                 300  
  
 Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile Glu Gly Val Thr His  
                  305                 310                 315                 320  
  
 Ala Leu Arg Thr Thr Glu Tyr His Asp Arg Asp Glu Gln Phe Tyr Trp  
                  325                 330                 335  
  
 Ile Ile Glu Ala Leu Gly Ile Arg Lys Pro Tyr Ile Trp Glu Tyr Ser  
                  340                 345                 350  
  
 Arg Leu Asn Leu Asn Asn Thr Val Leu Ser Lys Arg Lys Leu Thr Trp  
                  355                 360                 365  
  
 Phe Val Asn Glu Gly Leu Val Asp Gly Trp Asp Asp Pro Arg Phe Pro  
                  370                 375                 380  
  
 Thr Val Arg Gly Val Leu Arg Arg Gly Met Thr Val Glu Gly Leu Lys  
                  385                 390                 395                 400  
  
 Gln Phe Ile Ala Ala Gln Gly Ser Ser Arg Ser Val Val Asn Met Glu  
                  405                 410                 415  
  
 Trp Asp Lys Ile Trp Ala Phe Asn Lys Lys Val Ile Asp Pro Val Ala  
                  420                 425                 430  
  
 Pro Arg Tyr Val Ala Leu Leu Lys Lys Glu Val Ile Pro Val Asn Val  
                  435                 440                 445  
  
 Pro Glu Ala Gln Glu Glu Met Lys Glu Val Ala Lys His Pro Lys Asn  
                  450                 455                 460  
  
 Pro Glu Val Gly Leu Lys Pro Val Trp Tyr Ser Pro Lys Val Phe Ile  
                  465                 470                 475                 480  
  
 Glu Gly Ala Asp Ala Glu Thr Phe Ser Glu Gly Glu Met Val Thr Phe  
                  485                 490                 495  
  
 Ile Asn Trp Gly Asn Leu Asn Ile Thr Lys Ile His Lys Asn Ala Asp  
                  500                 505                 510  
  
 Gly Lys Ile Ile Ser Leu Asp Ala Lys Phe Asn Leu Glu Asn Lys Asp  
                  515                 520                 525  
  
 Tyr Lys Lys Thr Thr Lys Val Thr Trp Leu Ala Glu Thr Thr His Ala  
                  530                 535                 540  
  
 Leu Pro Ile Pro Val Ile Cys Val Thr Tyr Glu His Leu Ile Thr Lys  
                  545                 550                 555                 560  
  
 Pro Val Leu Gly Lys Asp Glu Asp Phe Lys Gln Tyr Val Asn Lys Asn  
                  565                 570                 575

Ser Lys His Glu Glu Leu Met Leu Gly Asp Pro Cys Leu Lys Asp Leu  
580 585 590

Lys Lys Gly Asp Ile Ile Gln Leu Gln Arg Arg Gly Phe Phe Ile Cys  
595 600 605

Asp Gln Pro Tyr Glu Pro Val Ser Pro Tyr Ser Cys Lys Glu Ala Pro  
610 615 620

Cys Val Leu Ile Tyr Ile Pro Asp Gly His Thr Lys Glu Met Pro Thr  
625 630 635 640

Ser Gly Ser Lys Glu Lys Thr Lys Val Glu Ala Thr Lys Asn Glu Thr  
645 650 655

Ser Ala Pro Phe Lys Glu Arg Pro Thr Pro Ser Leu Asn Asn Asn Cys  
660 665 670

Thr Thr Ser Glu Asp Ser Leu Val Leu Tyr Asn Arg Val Ala Val Gln  
675 680 685

Gly Asp Val Val Arg Glu Leu Lys Ala Lys Lys Ala Pro Lys Glu Asp  
690 695 700

Val Asp Ala Ala Val Lys Gln Leu Leu Ser Leu Lys Ala Glu Tyr Lys  
705 710 715 720

Glu Lys Thr Gly Gln Glu Tyr Lys Pro Gly Asn Pro Pro Ala Glu Ile  
725 730 735

Gly Gln Asn Ile Ser Ser Asn Ser Ser Ala Ser Ile Leu Glu Ser Lys  
740 745 750

Ser Leu Tyr Asp Glu Val Ala Ala Gln Gly Glu Val Val Arg Lys Leu  
755 760 765

Lys Ala Glu Lys Ser Pro Lys Ala Lys Ile Asn Glu Ala Val Glu Cys  
770 775 780

Leu Leu Ser Leu Lys Ala Gln Tyr Lys Glu Lys Thr Gly Lys Glu Tyr  
785 790 795 800

Ile Pro Gly Gln Pro Pro Leu Ser Gln Ser Ser Asp Ser Ser Pro Thr  
805 810 815

Arg Asn Ser Glu Pro Ala Gly Leu Glu Thr Pro Glu Ala Lys Val Leu  
820 825 830

Phe Asp Lys Val Ala Ser Gln Gly Glu Val Val Arg Lys Leu Lys Thr  
835 840 845

Glu Lys Ala Pro Lys Asp Gln Val Asp Ile Ala Val Gln Glu Leu Leu  
850 855 860

Gln Leu Lys Ala Gln Tyr Lys Ser Leu Ile Gly Val Glu Tyr Lys Pro  
865 870 875 880

Val Ser Ala Thr Gly Ala Glu Asp Lys Asp Lys Lys Lys Glu Lys  
885 890 895

Glu Asn Lys Ser Glu Lys Gln Asn Lys Pro Gln Lys Gln Asn Asp Gly  
 900 905 910  
 Gln Arg Lys Asp Pro Ser Lys Asn Gln Gly Gly Gly Leu Ser Ser Ser  
 915 920 925  
 Gly Ala Gly Glu Gly Gln Gly Pro Lys Lys Gln Thr Arg Leu Gly Leu  
 930 935 940  
 Glu Ala Lys Lys Glu Glu Asn Leu Ala Asp Trp Tyr Ser Gln Val Ile  
 945 950 955 960  
 Thr Lys Ser Glu Met Ile Glu Tyr His Asp Ile Ser Gly Cys Tyr Ile  
 965 970 975  
 Leu Arg Pro Trp Ala Tyr Ala Ile Trp Glu Ala Ile Lys Asp Phe Phe  
 980 985 990  
 Asp Ala Glu Ile Lys Lys Leu Gly Val Glu Asn Cys Tyr Phe Pro Met  
 995 1000 1005  
 Phe Val Ser Gln Ser Ala Leu Glu Lys Glu Lys Thr His Val Ala Asp  
 1010 1015 1020  
 Phe Ala Pro Glu Val Ala Trp Val Thr Arg Ser Gly Lys Thr Glu Leu  
 1025 1030 1035 1040  
 Ala Glu Pro Ile Ala Ile Arg Pro Thr Ser Glu Thr Val Met Tyr Pro  
 1045 1050 1055  
 Ala Tyr Ala Lys Trp Val Gln Ser His Arg Asp Leu Pro Ile Lys Leu  
 1060 1065 1070  
 Asn Gln Trp Cys Asn Val Val Arg Trp Glu Phe Lys His Pro Gln Pro  
 1075 1080 1085  
 Phe Leu Arg Thr Arg Glu Phe Leu Trp Gln Glu Gly His Ser Ala Phe  
 1090 1095 1100  
 Ala Thr Met Glu Glu Ala Ala Glu Glu Val Leu Gln Ile Leu Asp Leu  
 1105 1110 1115 1120  
 Tyr Ala Gln Val Tyr Glu Glu Leu Leu Ala Ile Pro Val Val Lys Gly  
 1125 1130 1135  
 Arg Lys Thr Glu Lys Glu Lys Phe Ala Gly Gly Asp Tyr Thr Thr Thr  
 1140 1145 1150  
 Ile Glu Ala Phe Ile Ser Ala Ser Gly Arg Ala Ile Gln Gly Gly Thr  
 1155 1160 1165  
 Ser His His Leu Gly Gln Asn Phe Ser Lys Met Phe Glu Ile Val Phe  
 1170 1175 1180  
 Glu Asp Pro Lys Ile Pro Gly Glu Lys Gln Phe Ala Tyr Gln Asn Ser  
 1185 1190 1195 1200  
 Trp Gly Leu Thr Thr Arg Thr Ile Gly Val Met Thr Met Val His Gly  
 1205 1210 1215

Asp Asn Met Gly Leu Val Leu Pro Pro Arg Val Ala Cys Val Gln Val  
1220 1225 1230

Val Ile Ile Pro Cys Gly Ile Thr Asn Ala Leu Ser Glu Glu Asp Lys  
1235 1240 1245

Glu Ala Leu Ile Ala Lys Cys Asn Asp Tyr Arg Arg Arg Leu Leu Ser  
1250 1255 1260

Val Asn Ile Arg Val Arg Ala Asp Leu Arg Asp Asn Tyr Ser Pro Gly  
1265 1270 1275 1280

Trp Lys Phe Asn His Trp Glu Leu Lys Gly Val Pro Ile Arg Leu Glu  
1285 1290 1295

Val Gly Pro Arg Asp Met Lys Ser Cys Gln Phe Val Ala Val Arg Arg  
1300 1305 1310

Asp Thr Gly Glu Lys Leu Thr Val Ala Glu Asn Glu Ala Glu Thr Lys  
1315 1320 1325

Leu Gln Ala Ile Leu Glu Asp Ile Gln Val Thr Leu Phe Thr Arg Ala  
1330 1335 1340

Ser Glu Asp Leu Lys Thr His Met Val Val Ala Asn Thr Met Glu Asp  
1345 1350 1355 1360

Phe Gln Lys Ile Leu Asp Ser Gly Lys Ile Val Gln Ile Pro Phe Cys  
1365 1370 1375

Gly Glu Ile Asp Cys Glu Asp Trp Ile Lys Lys Thr Thr Ala Arg Asp  
1380 1385 1390

Gln Asp Leu Glu Pro Gly Ala Pro Ser Met Gly Ala Lys Ser Leu Cys  
1395 1400 1405

Ile Pro Phe Lys Pro Leu Cys Glu Leu Gln Pro Gly Ala Lys Cys Val  
1410 1415 1420

Cys Gly Lys Asn Pro Ala Lys Tyr Tyr Thr Leu Phe Gly Arg Ser Tyr  
1425 1430 1435 1440